

New record of *Geopora sumneriana* from Pakistan

IRFANA MAQSAD, BARKAT ALI,
TASMIA BASHIR, ABDUL SAMAD MUMTAZ*

*Department of Plant Sciences, Faculty of Biological Sciences, Quaid-i-Azam University,
Islamabad, 45320, Pakistan*

*CORRESPONDENCE TO: asmumtaz@qau.edu.pk

ABSTRACT—A new record of *Geopora sumneriana* is presented from Pakistan. Specimens were collected under *Cedrus deodara* trees in Chitral district of Khyber Pakhtunkhwa province during 2018. The newly reported specimens are illustrated and described using morphological characters and phylogenetic analysis of the internal transcribed spacer region (ITS).

KEY WORDS—cup fungi, *Pezizales*, phylogeny, *Pyronemataceae*, taxonomy

Introduction

Geopora Harkn. (*Pyronemataceae*, *Pezizales*) was established by Harkness (1885) based on the hypogeous type species *Geopora cooperi* Harkn. With the addition of semihypogeous and epigeous species, the genus has since been expanded to 27 species and six infraspecific taxa (Index Fungorum 2020). Five species—*G. arenosa* (Fuckel) S. Ahmad, *G. foliacea* (Schaeff.) S. Ahmad, *G. arenicola* (Lév.) Kers, *G. cooperi*, and *G. ahmadii* Saba & al.—have been reported from Pakistan (Ashraf & Khalid 2012, Saba & al. 2019).

Geopora taxa are morphologically characterized by ascomata that are partially or completely subterranean and covered with flexible, thin or thick, septate excipular hairs; a whitish, greyish or yellowish grey hymenium; an excipulum divided into two (the ectal and medullary) layers; operculate cylindrical asci; uniseriate, ellipsoid or ellipsoidal-

fusiform, predominantly smooth (although *G. lateritia* (Fogel & States) Healy & M.E. Sm. has ornamented spores; Grupe & al. 2019) ascospores with one or two guttules (Tamm & al. 2010, Perić & Perić 2011). *Geopora* species fruit on soil, sand, or often rotten and decaying plant materials and form ectomycorrhizal relationships with trees (Tamm & al. 2010).

Tamm & al. (2010) concluded that previously used taxonomic characters—such as ascospore size, hymenial color, ectomycorrhizal relationships, ascomatal shape and position, and ploidy level—are insufficient for circumscribing *Geopora* species. Similarly, geographic research data also do not help in delimiting species within the genus. An integrative approach to taxonomy combining morphological and DNA sequence data—as applied in many other groups of fungi (e.g., Ko & al. 2011, Stefani & al. 2014, Ali & al. 2016, Skrede & al. 2017, Sousa & al. 2017, Haelewaters & al. 2018, Song & al. 2019)—has been suggested for classifying species within *Geopora* (Tamm & al. 2010, Flores-Rentería & al. 2014). The description of *G. ahmadii*, for example, was supported by both morphological and molecular phylogenetic data (Saba & al. 2019).

During our macrofungal field surveys, we collected some gregarious specimens of *Geopora* on moist soil under *Cedrus deodara* (Roxb. ex D. Don) G. Don trees in Chitral District, Northern Pakistan. Our preliminary field observations, morphological examinations, and ITS sequence data identified the specimens as *G. sumneriana*, which constitutes the first report of this species in Pakistan.

Materials & methods

Microscopic study

The specimens collected in the Chitral district were dried in a food dehydrator at 40 °C for 8 hours. Microscopic characters were measured and photographed using a Leitz light microscope and Leica camera. Fungal tissues were mounted in water, KOH, and Congo red. The specimens were deposited in the herbarium of Plant Sciences Department, Quaid-i-Azam University, Islamabad, Pakistan (ISL).

DNA extraction, PCR amplification, DNA sequencing

DNA was extracted from a small section of the dried apothecium using a modified CTAB protocol (O'Donnell & al. 2009). The internal transcribed spacer region (ITS) was amplified with the primer pair ITS1F and ITS4 (White & al. 1990, Gardes & Bruns 1993). PCR parameters were set as follows: initial denaturation at 95 °C for 5 min, followed by 38 cycles of denaturation at 95 °C for 30 s, annealing at 56 °C for 40 s, and extension at 72 °C for 1:30 min; and a final extension at 72 °C for 10 min. The PCR product was purified using the Thermo Scientific™ GeneJET PCR

TABLE 1. Geopora species and outgroup species used in the phylogenetic analyses. The newly generated sequence is presented in bold font.

TAXA	COUNTRY	VOUCHER/ ISOLATE/STRAIN	ITS	REFERENCES
<i>Geopora ahmadii</i>	Pakistan	MSM0091	KY805995	Saba & al. 2019
	Pakistan	MSM00163	KY805996	Saba & al. 2019
<i>G. arenicola</i>	Finland	H SJ-4366	FM206457	Tamm & al. 2010
	Finland	TAA 188638	FM206453	Tamm & al. 2010
	Finland	H VH23012	FM206454	Tamm & al. 2010
	Finland	H VH22603	FM206455	Tamm & al. 2010
	Estonia	TAAM 192325	FM206456	Tamm & al. 2010
<i>G. cervina</i>	Estonia	TAA 188304	FM206417	Tamm & al. 2010
	Estonia	TAA 117898	FM206419	Tamm & al. 2010
	Estonia	TAA 188517	FM206418	Tamm & al. 2010
<i>G. cercocarp</i>	USA	Kropp2	HQ283097	Southworth & Frank 2011
	USA	Kropp1	HQ283096	Southworth & Frank 2011
	USA	SOC1596	HQ283094	Southworth & al. 2011
<i>G. clausa</i>	USA	OSC 58245	MK359192	Grupe & al. 2019
<i>G. cooperi</i>	Spain	101GA	AF387651	Gutierrez & al. (unpubl.)
	Spain	108GC	AF387649	Gutierrez & al. (unpubl.)
	Spain	109GC	AF387650	Gutierrez & al. (unpubl.)
<i>G. foliacea</i>	Finland	H RS-34685	FM206428	Tamm & al. 2010
	Finland	H RS-29584	FM206424	Tamm & al. 2010
<i>G. gilkeyae</i>	USA, CA	src515	DQ974731	Smith & al. 2007
<i>G. pinyonensis</i>	USA, AR	DGB 27586	KF768652	Flores-Renteria & al. 2014
	USA, AR	DGB 27586	KF768653	Flores-Renteria & al. 2014
<i>G. sepulta</i>	Estonia	TAA 192333	FM206431	Tamm & al. 2010
	Estonia	TAA 192311	FM206432	Tamm & al. 2010
<i>G. summeriana</i>	Pakistan	ISL99125	MN860070	This paper
	India	RS-18-1000	MN200944	Sharma (unpubl.)
	Italy	16978	JF908024	Osmundson & al. 2013
<i>G. tenuis</i>	Finland	H RS-09584	FM206402	Tamm & al. 2010
	Estonia	TAA 188326	FM206397	Tamm & al. 2010
	Estonia	TAA 188331	FM206396	Tamm & al. 2010
<i>G. tolucana</i>	USA	375	MK842019	Shemesh & al. (unpubl.)
	USA	217	MK841861	Shemesh & al. (unpubl.)
	USA	376	MK842020	Shemesh & al. (unpubl.)
	USA	222	MK841866	Shemesh & al. (unpubl.)
	USA	215	MK841859	Shemesh & al. (unpubl.)
<i>Trichophaea hybrida</i>	Estonia	TAA 192334	FM206477	Tamm & al. 2010
<i>Tarzettia catinus</i>	Estonia	TAA 192291	FM206478	Tamm & al. 2010

purification kit according to the manufacturer's instructions and commercially sequenced by Macrogen (Korea).

Phylogenetic analysis

The raw sequence reads were manually assembled, checked, and corrected in CLC Main Workbench version 8.1 (QIAGEN Aarhus A/S). The ITS sequence dataset included 37 sequences, including 34 *Geopora* sequences downloaded from NCBI GenBank, one sequence generated during the present study, and two outgroup sequences (*Tarsetta catinus* (Holmsk.) Korf & J.K. Rogers and *Trichophaea hybrida* (Sowerby) T. Schumach.) also downloaded from GenBank (TABLE 1). The ITS dataset was aligned using the Muscle E multiple alignment tool in MEGA v. 7.0 (Kumar & al. 2016). Gaps and missing data were excluded from the dataset.

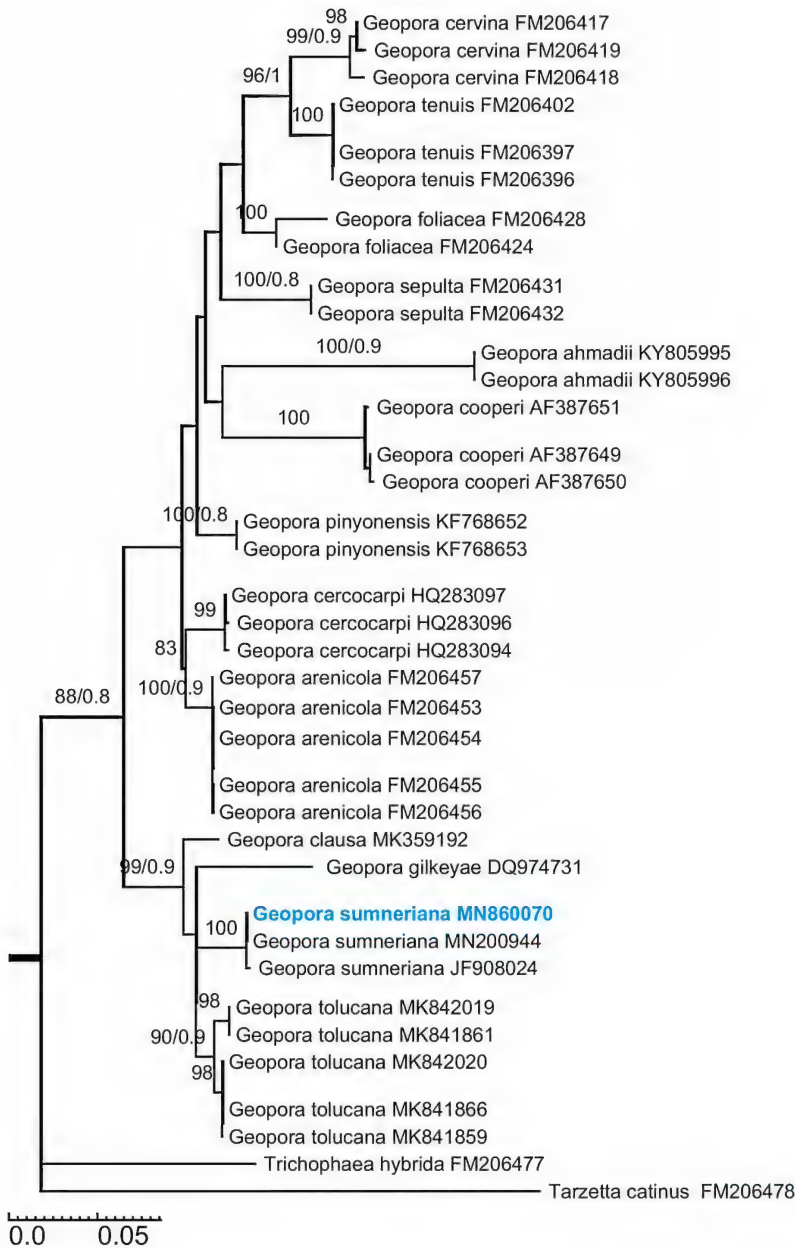
The best-fit nucleotide substitution model was chosen from the model test tool in MEGA 7.0 (Kumar & al. 2016) using the Akaike Information Criterion (AIC). The phylogeny of the ITS sequences was constructed using maximum likelihood inference (ML) under the General Time Reversible Model of nucleotide substitution (GTR + I + Γ ; Nei & Kumar 2000). Bootstrap support values were obtained from 1000 replications. A heuristic search was performed on the matrix of pairwise distances using maximum composite likelihood method of estimation and Neighbor-Joining and BioNJ algorithms. MEGA 7.0 (Kumar & al. 2016) was used for the phylogenetic analysis. The final tree was visualized and formatted in FigTree v.1.4.4 and TreeGraph 2.0 (FIG. 1).

Bayesian inference with Metropolis-coupled Markov Chain Monte Carlo (MCMC) method was used to estimate posterior probabilities in MrBayes version 3.2.7a (Ronquist & al. 2012). The nucleotide substitution model selected was GTR + I + Γ . The analysis was carried out in two runs and four chains, each with 1,000,000 generations. The temperature (1.0) was used for the cold chain. The MCMC model parameters were adjusted to every 500 generations and trees were sampled every 1000 generations. A default burn-in of 25% was used by MrBayes to discard samples from the cold chain and 3020 trees were summarized to construct a consensus tree. Bayesian posterior probability values of >0.8 were used in the final fit-tree.

Phylogenetic results

Our query sequence Blast produced the highest hits for *Geopora sumneriana* from Italy (JF908024, 99.82 identity) and *G. sumneriana* from India (MN200944,

FIGURE 1. A phylogram of *Geopora* species constructed from ITS sequences. Maximum likelihood (ML) and Bayesian inference (BI) methods of phylogeny were conducted in MEGA 7.0 and MrBayes 3.2.7a. Bootstrap probability values $>80\%$ and posterior probability values ≥ 0.80 are shown above the branches. *Geopora sumneriana*, investigated in this paper, stands in blue font. *Tarsetta catinus* and *Trichophaea hybrida* represent outgroup taxa.



100 identity). *Tarzetia catinus* and *Trichophaea hybrida* were chosen for rooting purpose due to their close phylogenetic relationship with *Geopora* species (Perry & al. 2007, Saba & al. 2019). The best tree recovered from ML analysis ($-\ln L = 1925.2196$) is shown in FIG. 1. Our *G. sumneriana* ITS sequence clusters with the *G. sumneriana* sequences from Italy and India (FIG. 1) in a clade with 100% ML bootstrap support; however, Bayesian inference support was only moderate (posterior probability = 0.65).

Taxonomy

Geopora sumneriana (Cooke ex W. Phillips) M. Torre,

Anales Inst. Bot. Cavanilles 32(2): 96. 1976 ["1975"].

PLATES 1, 2

APOTHECIUM large, sessile, outer surface brown or deep brown, covered with fine hairs and dust particles, scaly, rough, brittle, at first subterranean and globular in shape, closed, upon maturity a small opening arising at the top with regular margins, later breaking through soil, then margins splitting into 4–6 lobes or rays, resembling star or crown-shape, then making a wide bowl shape; at maturity semihypogeous or partially immersed in the soil; stem absent, apothecium attached to the substrate through a tiny tubular structure in the center or brown mycelium. HYMENIUM deeply concave, smooth, whitish and at maturity creamy or pale beige color. ASCUS hyaline, eight-spored, operculate, cylindrical, $182\text{--}300 \times 16\text{--}27\text{ }\mu\text{m}$, rounded at the top ($16\text{--}27\text{ }\mu\text{m}$ diam.), narrower at the base ($6\text{--}8\text{ }\mu\text{m}$ diam.). ASCOSPORES ellipsoid and fusiform, uniseriate, sometimes containing two larger oil drops and many small oil drops around them, or mostly one oil drop, $28\text{--}33 \times 12.9\text{--}15\text{ }\mu\text{m}$, hyaline, smooth, thick walled, colorless in water, in Melzer's reagent no change in color observed. PARAPHYSES thread-like and narrow, cylindrical, hyaline, broader at the middle $\leq 3\text{--}4\text{ }\mu\text{m}$ diam., slightly enlarged at the top $\leq 4\text{--}6\text{ }\mu\text{m}$ diam., septate. ECTAL EXCIPULUM is textura globuloso-angularis, made up of oval or irregular shaped cells, $17.5\text{--}42.5 \times 10\text{--}28\text{ }\mu\text{m}$, transparent or brown at the surface. HAIRS arising from ectal excipulum, septate, lighter or darker brown, thick-walled, blunt ends and rounded, very long, $12\text{--}15\text{ }\mu\text{m}$ diam., cytoplasm with numerous crystals. ANCHOR HYPHAE septate, dense, very long, light brownish and curled with rounded ends.

PLATE 1. *Geopora sumneriana* (ISL99125): A, B. Maturing and immature apothecia; C. Asci and paraphyses; D. Ascus; E. Ascus with ascospores, some ascospores with only one large oil drop and others with two oil drops, one large and one small; F. Ectal excipulum cells; G. Hyphae; H. Septate paraphyses; I. Excipular hairs with base. Scale bars: C = $200\text{ }\mu\text{m}$; F = $50\text{ }\mu\text{m}$; G–I = $20\text{ }\mu\text{m}$.



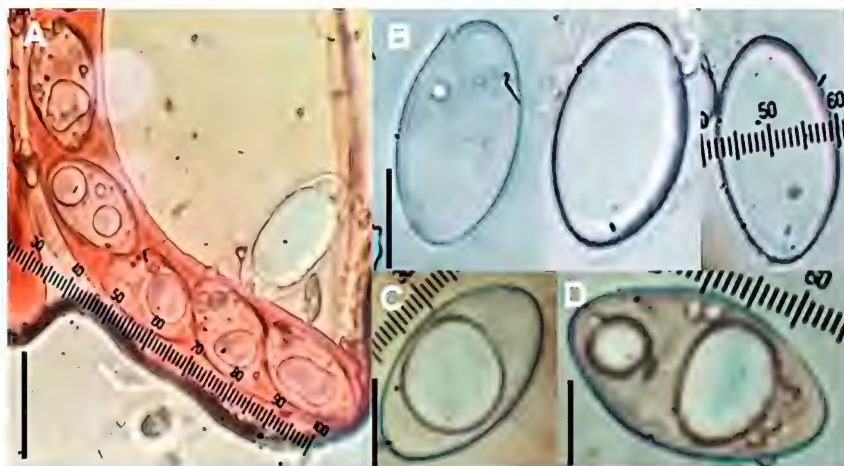


PLATE 2. *Geopora sumneriana* (ISL99125): A. Part of ascus showing ascospores with guttules; B. Ascospores without guttules, showing the ellipsoidal shape; C. Ascospore with one guttule; D. Ascospore with two guttules. Scale bars: A = 200 µm; B–D = 20 µm.

HABITAT In small groups, on moist ground beneath cedar (*Cedrus deodara*) and among the rotten cedar needles.

MATERIAL EXAMINED—PAKISTAN, KHYBER PAKHTUNKHWA PROVINCE, Chitral, Booni Gol Qasumandeh, collected beneath *Cedrus deodara*, alt. 2159 m a.s.l., 19 April 2018, leg. I. Maqсад (ISL99125; GenBank MN860070).

Discussion

In the present study, we discovered that our specimens closely match the original and subsequently published descriptions and illustrations of *Geopora sumneriana* (and its synonyms), a species widely known from Europe (Phillips 1887, Berkeley & Broome 1866, Yao & Spooner 1996, Perić & Perić 2011). The identification of our material as *G. sumneriana* is supported by BLAST matches with *G. sumneriana* sequences from India and Italy and our phylogenetic analysis (FIG. 1). This represents the first report of *G. sumneriana* from Pakistan.

The distinguishing characters of *G. sumneriana* include relatively large apothecia and asci, ellipsoid and fusiform ascospores (usually with two oil drops) measuring $(26.7\text{--})28.7\text{--}31.6\text{--}(32.1) \times (13.2\text{--})14.7\text{--}16.0\text{--}(16.3) \mu\text{m}$ (Torre 1975), and a habit under coniferous trees in spring (Phillips 1887, Perić & Perić 2011).

However, we did observe one difference in the morphological characters of our Pakistani material. Perić & Perić (2011) mention that the ascospores of *G. sumneriana* generally contain two oil drops but rarely one, whereas we observed generally one, rarely two oil drops in our specimens, potentially due to differences in developmental stage; our specimens appeared to be relatively young to immature (PLATE 2).

Geopora sumneriana and *G. arenosa* possess a similar ascospore spore size and shape; however, *G. arenosa* can be distinguished by its smaller apothecia (c. 15 mm diam. in *G. arenosa* vs. >30 mm diam), its phenology (late summer to autumn), and association with pine; Yao & Spooner 1996, 2003) instead of cedar. Also, the ascospore size and shape of our specimen was larger than in *G. arenosa* (25–29 × 12.5 µm; Yao & Spooner 2003). As no sequence data have been obtained from *G. arenosa*; efforts to re-collect and sequence specimens of this species would help elucidate its placement among related *Geopora* species.

The morphological species concept in *Geopora*, as in many other fungal groups, potentially leads to incorrect species identification of the species, primarily due to overlapping morphologies and rarity of fruiting bodies (Tamm & al. 2010, Flores-Rentería & al. 2014, Saba & al. 2019). Our phylogeny clustered our ITS sequence in a distinct clade with two other *G. sumneriana* sequences ML support 100% (FIG. 1). One nucleotide separated our ITS sequence and the *G. sumneriana* sequence from Italy (position 114). Additional collections and sequences from *G. sumneriana* might indicate intraspecific variations in the ITS region (e.g., Nilsson & al. 2008). *Geopora ahmadii* (Saba & al. 2019), morphologically similar to our *G. sumneriana*, is phylogenetically separated in our analysis (FIG. 1). Morphologically, *G. ahmadii* differs from *G. sumneriana* by single oil drop per ascospore and shorter length (19–26.0 µm long in *G. ahmadii*). Saba & al. (2019) hypothesized (based on ascospore size and shape) that *G. arenosa* collected from Pakistan might represent *G. ahmadii*. This should be tested by morphological examination and sequencing of the type specimen, as it is of supreme importance to evaluate type material to evaluate whether the name-bearing type material resembles or differs from newly collected samples (Dayarathne & al. 2016). Re-examination of type materials would definitely lead to more reliable identification of the species within *Geopora*.

In conclusion, informative field surveys and a combined approach involving thorough morphology and multi-locus phylogenetic analyses will help to resolve systematics and evolution of the species within *Geopora*.

Association of *Geopora* species with their ectomycorrhizal hosts, phenology, distribution, soil characteristics, and type specimens should also be studied to support correct species identifications.

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